

565760" OT 296E61 Fig. 1

1 CCACGGCGTC CGATAAATC AGCAGCGGC CGGAGAACCC CGCAATCTCT GCGCCACAA AATACACCGA CCATGCCGA TCTACTTTAA GGGCTGAAC
GGGTGGCAG GCGATTAG TCGTGGCCG CCTCTTGG GCGTAGAGA GCGGGTGT TTATGTGCT GCTACGGCT AGATGAAT CCAGACTTTG

101 CCACGGGCGT GAGGACTAT AAGAGCGTTC CCTACCGCCA TGGAACAAC GCGCGGCG CTTGCGGGC CCGGAAAGG CACGGCCAG
GGTGGCGGA CTCTCGATA TTCTCGCAG GATGGCGGT ACCTGTCTG CCGGGCGG GRAGCCCG GGCCTTTTC GGCCTTTTC GTGCGGGT
M eIgluGlnar gIyGlnaAn AlaProAla laSerGlyal aArglysaRg HisGlyProGly

201 GACCCAGGGA GGGCGGGA GCGCGGCTG GGTCCGGGT CCCCAGACC CTTGTGCTCG TTGTGCTCG GTCTCTCTG TTGTGCTCG CTGAGTCTGC
CTGGGTCCCT CGCGGCCCT CCGTCCGGAC CCGAGGCCCA GGGTCTCTG GAACAGAGC AACAGCGG CCAGGACGAC AACAGAGTC GACTCAGACG

22 ProArgG1 uAlaArgGly AlaArgProG lyleuArgva lProLysThr LeuValLeu alValAla alValLeu LeuValserA laGluSerAla

301 TCTGATCACC CAACAAGACC TAGCTCCCA GCAGAGAGCG GCCCACAA ARAAGAGTC CAGCCCTCA GAGGATTGT GTCCACCTGG ACACCATATC
AGACTAGTGG CATCTCTAC CATCTCTAC GTGAGGAGT ATCAGGGGT CCGTCTCTG GGTCTCTCG GTCTCTCA GTCGGGAGT CTCCCTNACA CAGGTGACC TGTGCTATAG

55 LeuileThr GlnGlnAsp lGlnArgala AlaProGlnG lNlysArgse rSerProSer GluGlyLeuC ysProProG lYHisHisile

401 TCAGAAGACG GTAGAGATTG CATCTCTGC AATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGTGCACC AGGTGTGATT
AGCTCTCTGC CATCTCTAC CATCTCTAC GTGAGGAGT TTTATACCTG TCCTGATATC GTGAGTGACC TTTCTCTCG TTTCTCTCG ARAAGACGAA CCGAOGTGG TCACACTAA

88 SerGluAspG lYArgAspCy sIleSerCys lYsTyrglyG lNAspTyse rThrHisTrp AnaAspLeuL eupheCysLe uArgCysThr ArgCysAspSer

501 CAGGTGAAGT GGAGCTAAGT CCCTGCACA CCCTGCACA CAGACGAGT CAGTGTGTGT CAGTGCAG CAGTGTGTGT CCGGGAAGAA GATCTCTCTG AGATGTGCGG
GTCCACTCA CCTCGATTCA GGGACGTGT GTGTGCACA GTGCAGCTTC GTGCAGCTTC TTTCTCTCG ARAAGACGAA GCGTGTCTT CTAGAGGAC TCTACACGGC

122 GlyGluva lGluLeuSer ProCysThrT hrThrArgas nThrValCys GlnCysGluG lGlyThrPh eArgGluGlu AspSerProG lMeIcCysArg

601 GAAGTCCCGC ACAGGGTGT CAGAGGGAT GGTCAAGGT CAGTGTGTGT GGTGATTGTA CAGTGTGTGT CAGTGTGTGT TGTGTCCACA AAGATTCAGG CATCATCATC
CTTCAGGGTGT TGTCCACAG GGTCTCCCTA CAGTGTCCAG CCACTAACAT CCACTAACAT CCACTAACAT CCACTAACAT CCACTAACAT CCACTAACAT

155 LysCysArg ThrGlyCysP roArgGlyMe tVallysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerG lYlleIleIle

701 GGAGTCAAG TGTGAGCGGT AGTCTTGATT GTGGCTGTGT GTGGCTGTGT GTGGCTGTGT GTGGCTGTGT GTGGCTGTGT GTGGCTGTGT GTGGCTGTGT
CCTCAGTGT CAGTGTGT CAGTGTGT CAGTGTGT CAGTGTGT CAGTGTGT CAGTGTGT CAGTGTGT CAGTGTGT CAGTGTGT

188 GlyValThr alAlaAla lValleuile ValAlaValP heValCysly sSerLeuLeu TriplysLysv alleuProTy rLeuLysGly lIcCysSerGly

801 GTGGTGTGT GGCACCTGAG CAGTGTGACA GAGCTCACA CAGACCTGGG GGTGAGGACA ATGTCTCTCA ATGTCTCTCA ATGTCTCTCA ATGTCTCTCA
CAGCACCACC CAGTGTGACT CAGTGTGACT CAGTGTGACT CAGTGTGACT CAGTGTGACT CAGTGTGACT CAGTGTGACT CAGTGTGACT CAGTGTGACT

222 GlyGlyG lYAspProGlu ArgValAspA rgSerSerG lNArgProGly AlaGluAspA snValleuAs nGluIleVal SerIleLeuG lNProThrGln

901 GTCCCTGAG CAGGAAATGG AGTCCAGGA GCGAGCAG CCAACAGGTG TCAACATGTT GTCCCTGGG GTCCCTGGG GTCCCTGGG GTCCCTGGG
CCAGGGACTC GTCTTTACC TTTAGGTCTT CAGTGTGCTC CAGTGTGCTC CAGTGTGCTC CAGTGTGCTC CAGTGTGCTC CAGTGTGCTC CAGTGTGCTC

255 ValProGlu GlnGluMetG luValGlnG lUpProAlaGlu ProThrGlyv alAsnMetle uSerProGly GluSerGluH isLeuLeuG lUpProAlaGlu

1001 GGTGAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TGGCACTGAG ACTCTGAGAC AGTGTCTCGA TGACTTTGCA GACTTGGTGC
GACTTTTCCA GACTCTCTC CTCGACGAC CAGGCTGCTT TACTTCCACT AGGTGACTC TGAGACTCTG TCACGAGACT CTGAAACCT CTGAACCCAG

288 AlaGluArgS erGlnArgar gArgLeuLeu ValProAlaA snGluGlyas pProThrGlu ThrLeuArg lNcysPheAs pAspPheAla AspLeuValPro

1101 CCTTTGACTC CTGGAGCCG CTCATGAGGA AGTTGGGCGCT CATGACCAAT GAGATAAGG TGGCTAAGG TGAGGCAGCG GGCCACAGGG ACACCTTGTA
 322 GGAACCTGAG GACCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTTC ACGATTTCG ACTGCTGCGC CCGGTGTCCT TGTGGAACAT
 pheAsp8e rTTPgluPro leuMetArgL ysLeuGlyLe uMetAspAn gluileLysV alAlaLysAl aLunLaala aLylHisArga spThrLeuTyr
 1201 CAGCATGCTG ATAAAGTGG TCAACAAAC CGGCGAGAT GCGCTGCTCC ACACCTGCT GATGCGCTG GAGAGAGACT TGCCAAAGCAG
 355 ThrMetLeu ileLysTrp alaAnLysTh rGlyArgAsp AlaSerValH leThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln
 1301 AAGATTGAGG ACCACTTGT GAGCTCTGA AAGTTATGT ATCTAGAGG TAATGCAGAC TCTGCCWGT CCTAAGTGTG ATCTCTTCA GGAAGTGAGA
 388 LysileGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluG lYasnAlaAsp SerAlaXqqS eFDG*
 1401 CCTTCCCTGG TTACCTTTT TTCTGGA AAAA AAGACCTTTT TOGGCTTGAC CTGAGGTCAG TCATCTTTTC ACGGTGTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG
 1501 CCATCCAAAC TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCAATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT
 1601 GCTCGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTT TGGGATGTCA TTGTTTTTAC ACCACTTTT ACCACTTTT TATCCTAATG TAATGCTTT ATTTATTTAT
 1701 TTGGGCTACA TTGTAGATC CATCTACAA AAAAAAAA AAAAAAAG GCGGCGCGG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
 AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCGGCGG TCAGATCTCA CCTGGACGTC TTCCGAACCGG CCGTACCGG

Fig. 1 (cont.)

A 2.9

2 B 79.

Fab/Apr01

Fig. 3

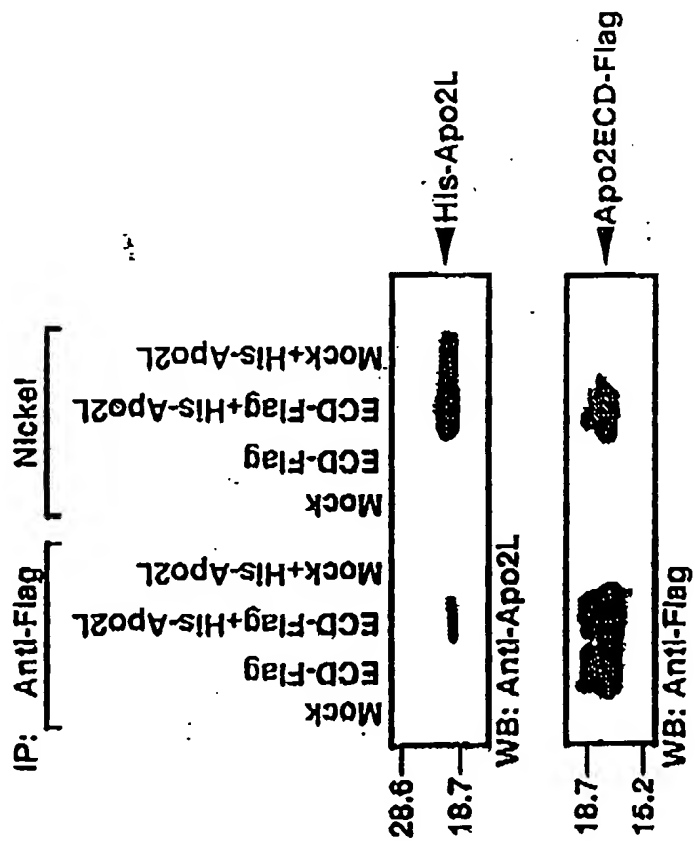


Fig. 4

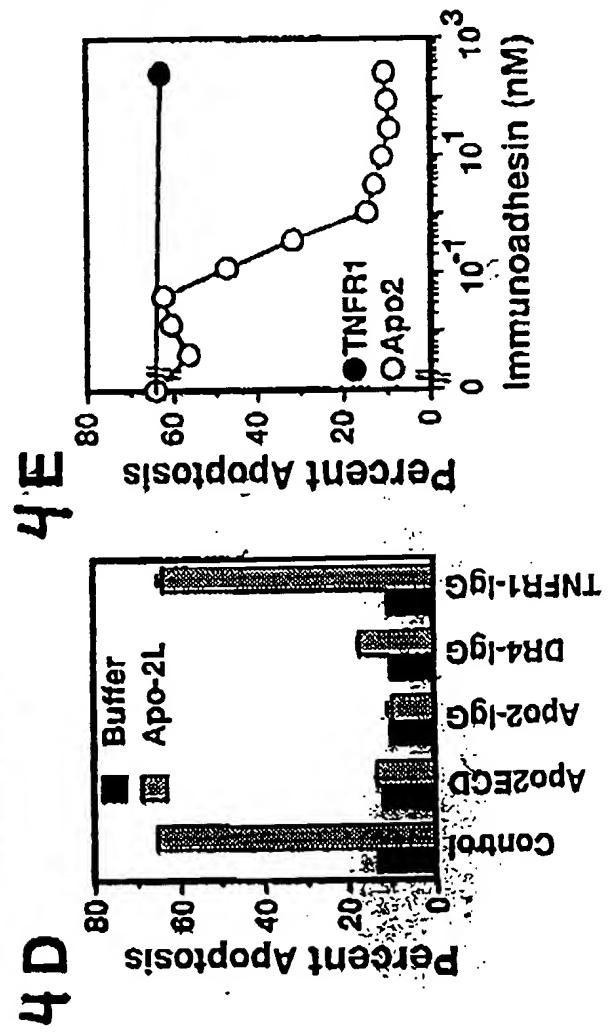
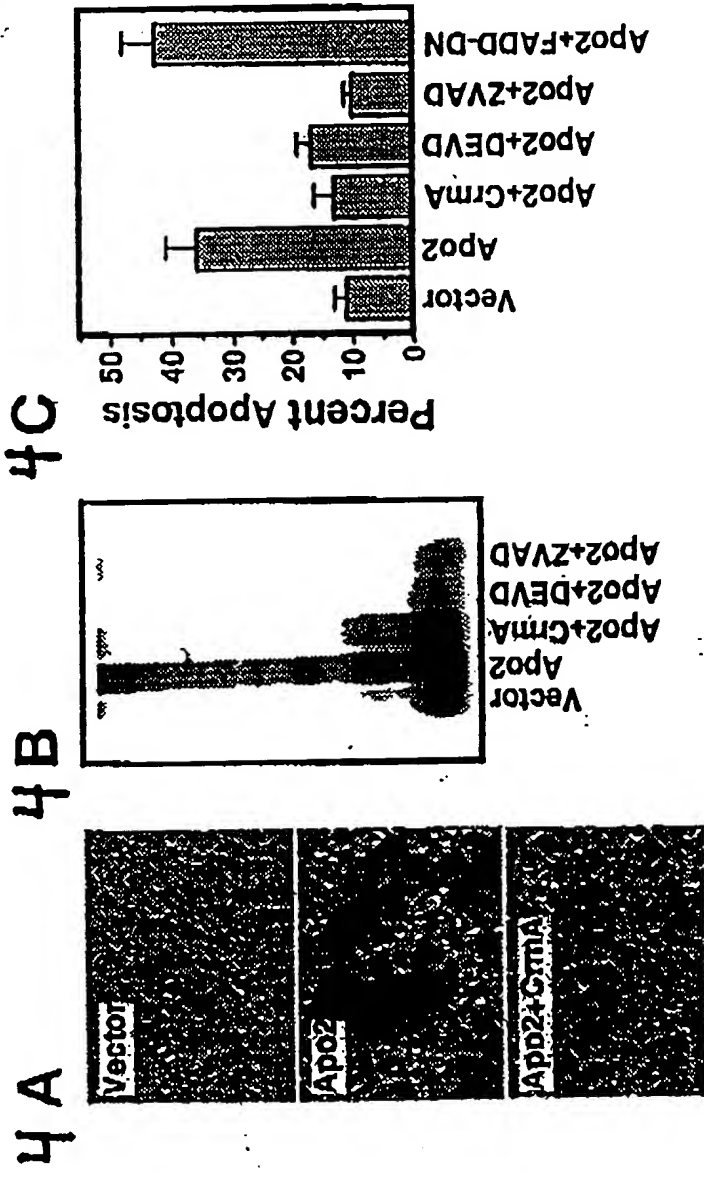
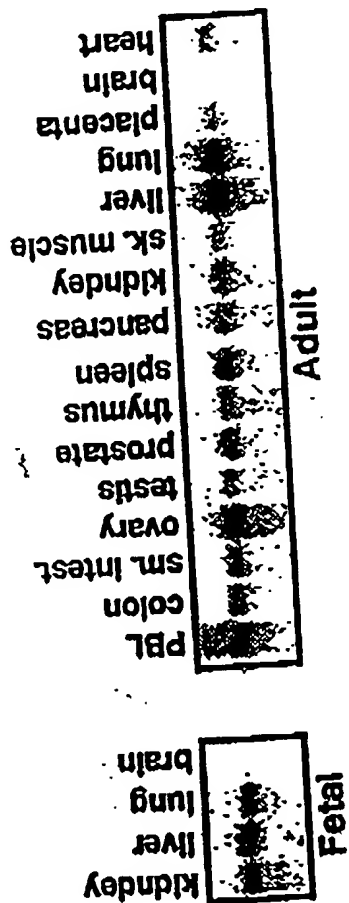


FIG. 6



655T60" 07/96E60

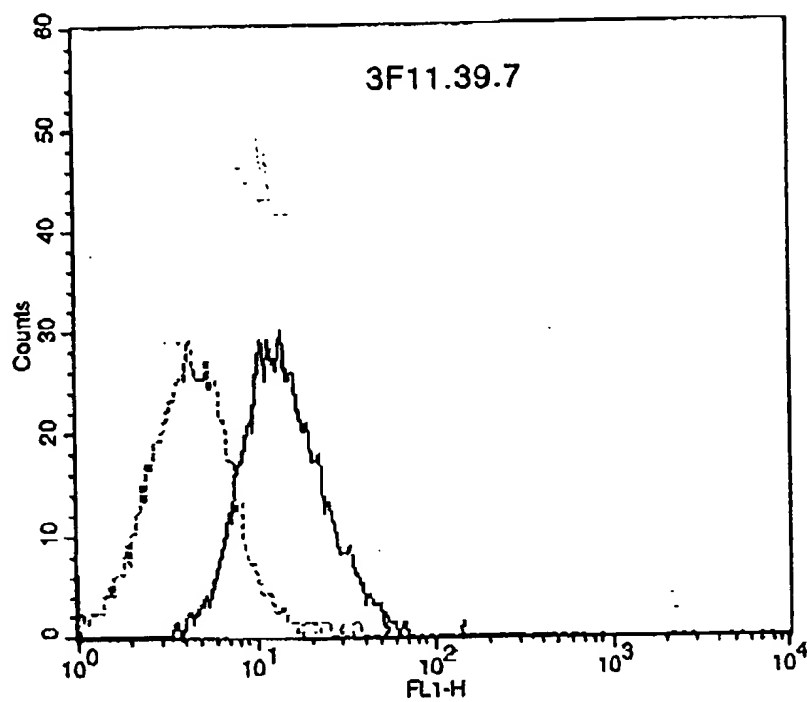


Fig. 7

005160" DT 296260

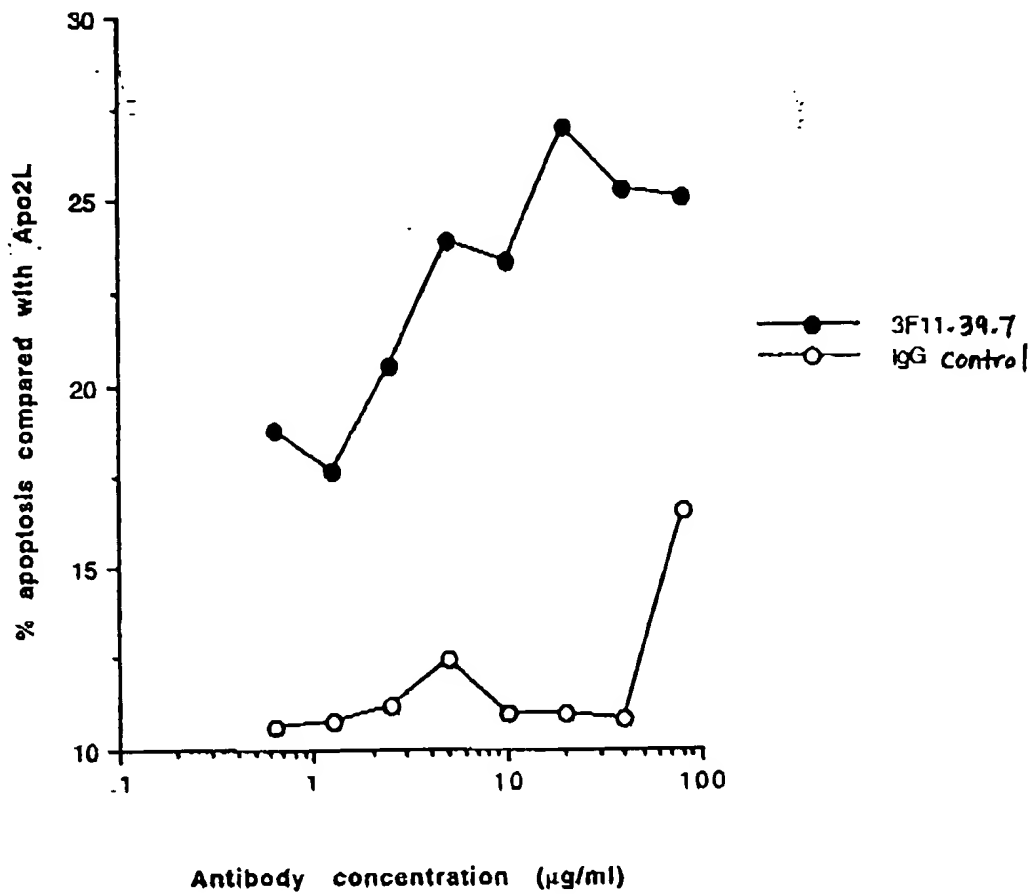


Fig. 8

0996710796660

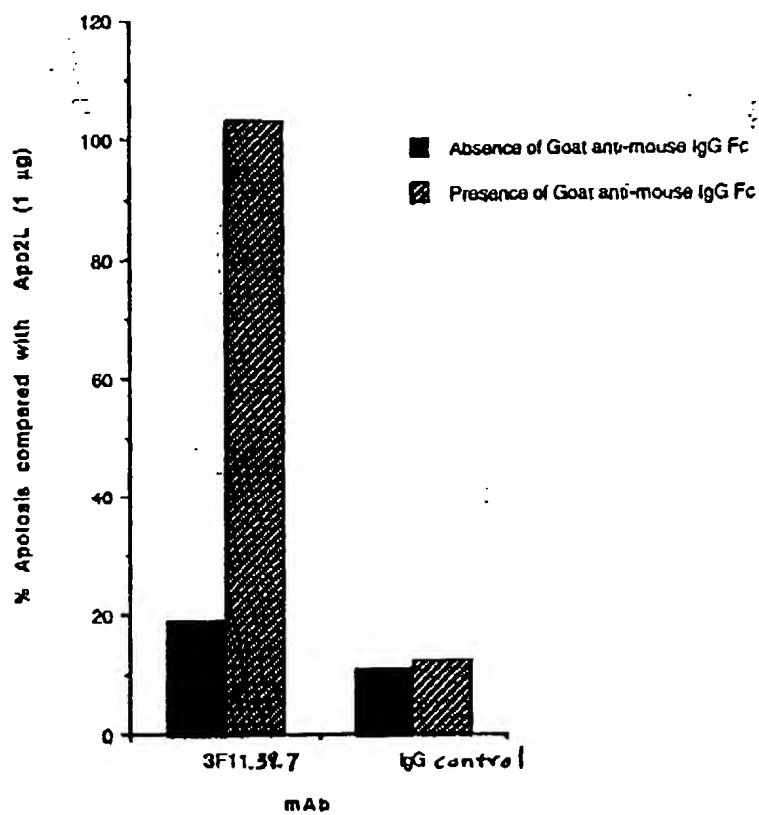


Fig. 9

09396710.091599
665160"07296260

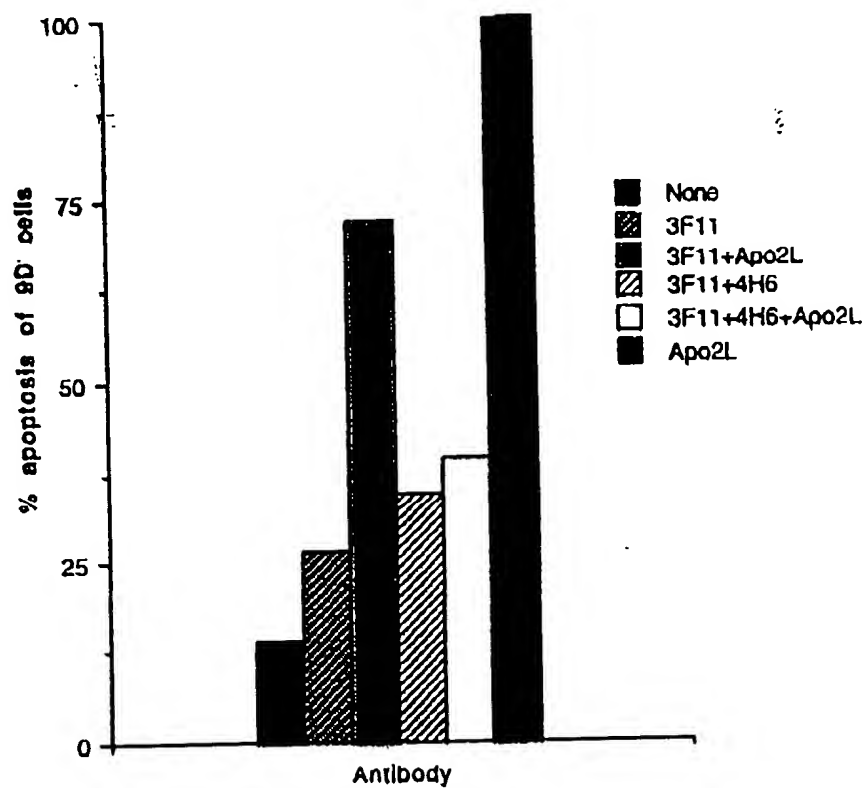


Fig : 10

665160" OF 296660

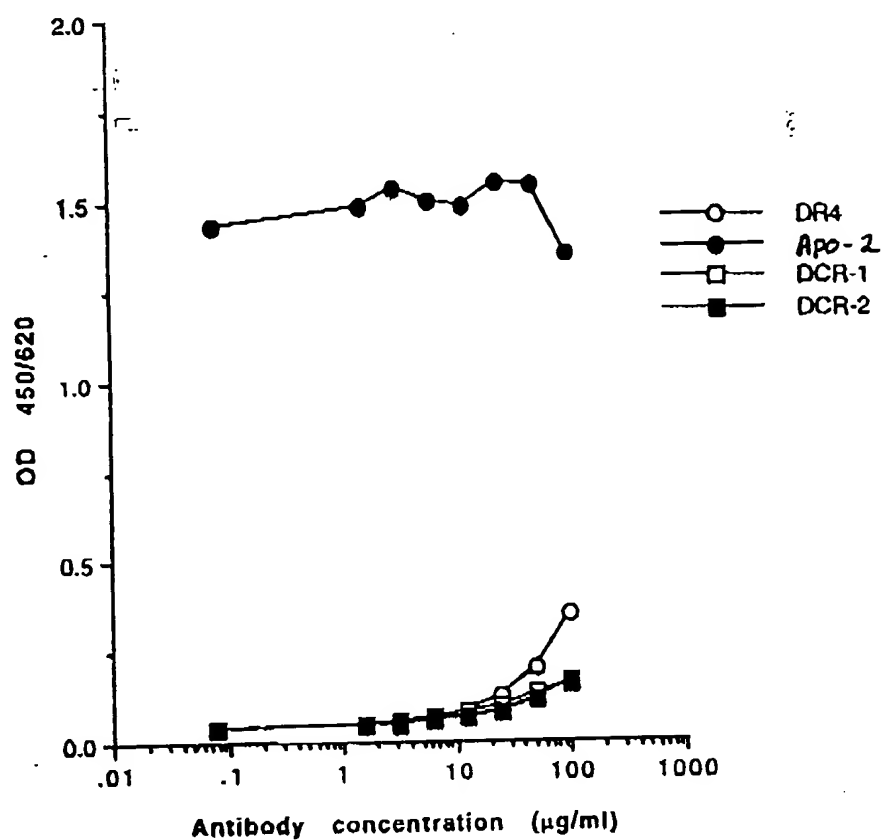


Fig. 11

Isotype	Kd-1 (pM)	Bloc	Apop w/L	Cross reactivity			IHC
				DR4	Apo-2	DCR1 DCR2	
2B3.7.1	20.	-	+	+	+++	-	+
3F11.39.7		+	+	-	+++	-	
4B9.23.6		-	+/-	-	+++	-	
5C7.9.1		-	+	+	+++	-	
3H1.18.10	4	-	-	+	+++	+/-	+
3H3.14.5		+	+	+	+++	+	+
3D5.1.10		-	+	++	+++	-	
3C9.8.6		+	+	-	+++	-	
4H10.14.10		+/-	?	+/-	+++	+/-	

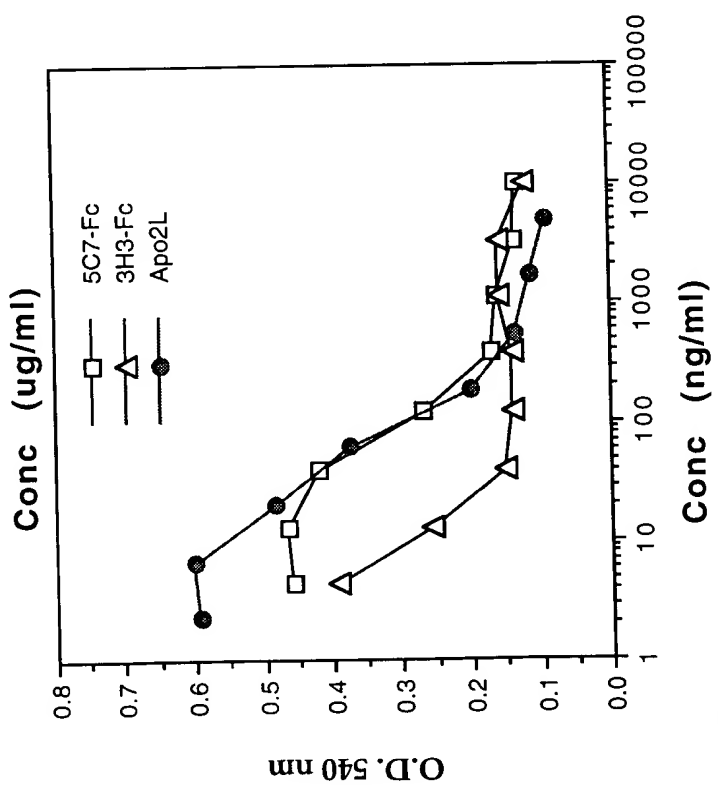
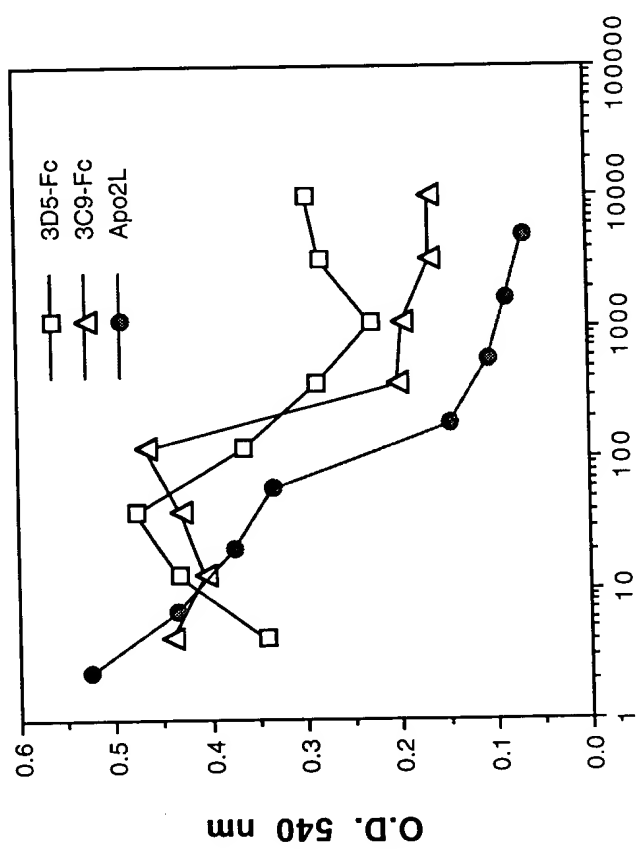
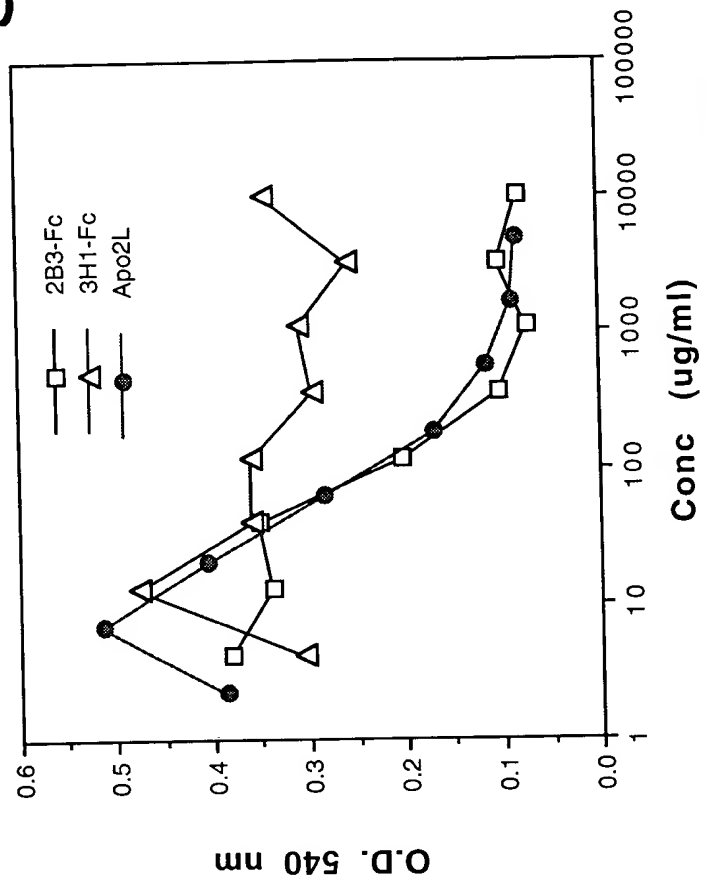
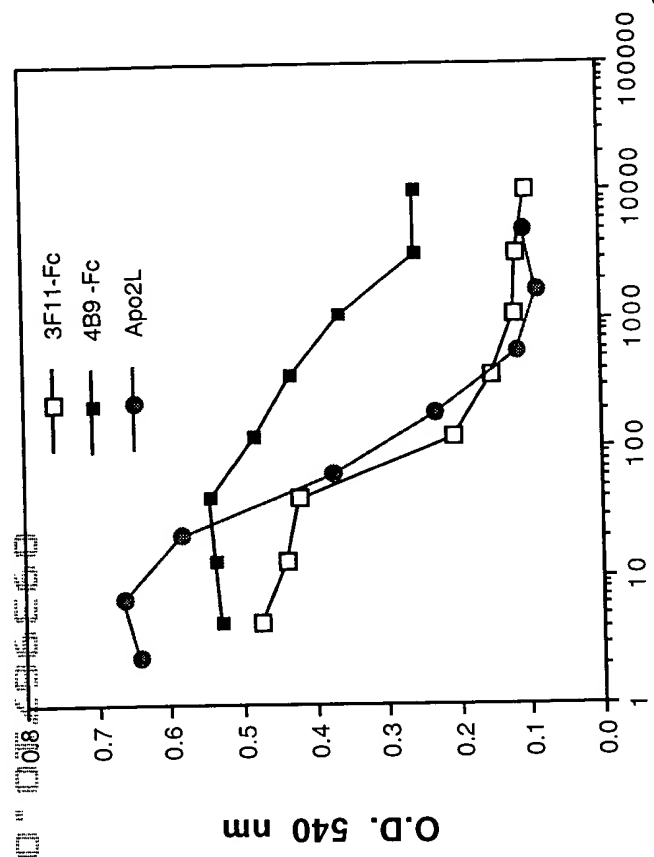
Fig. 12

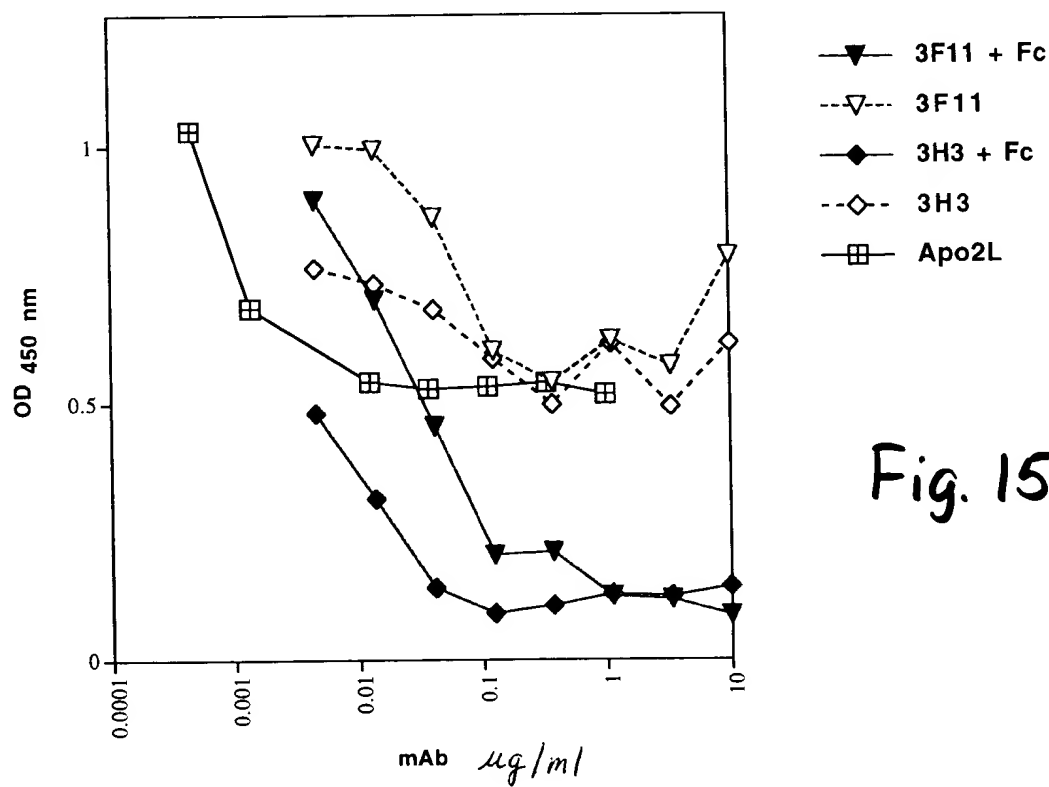
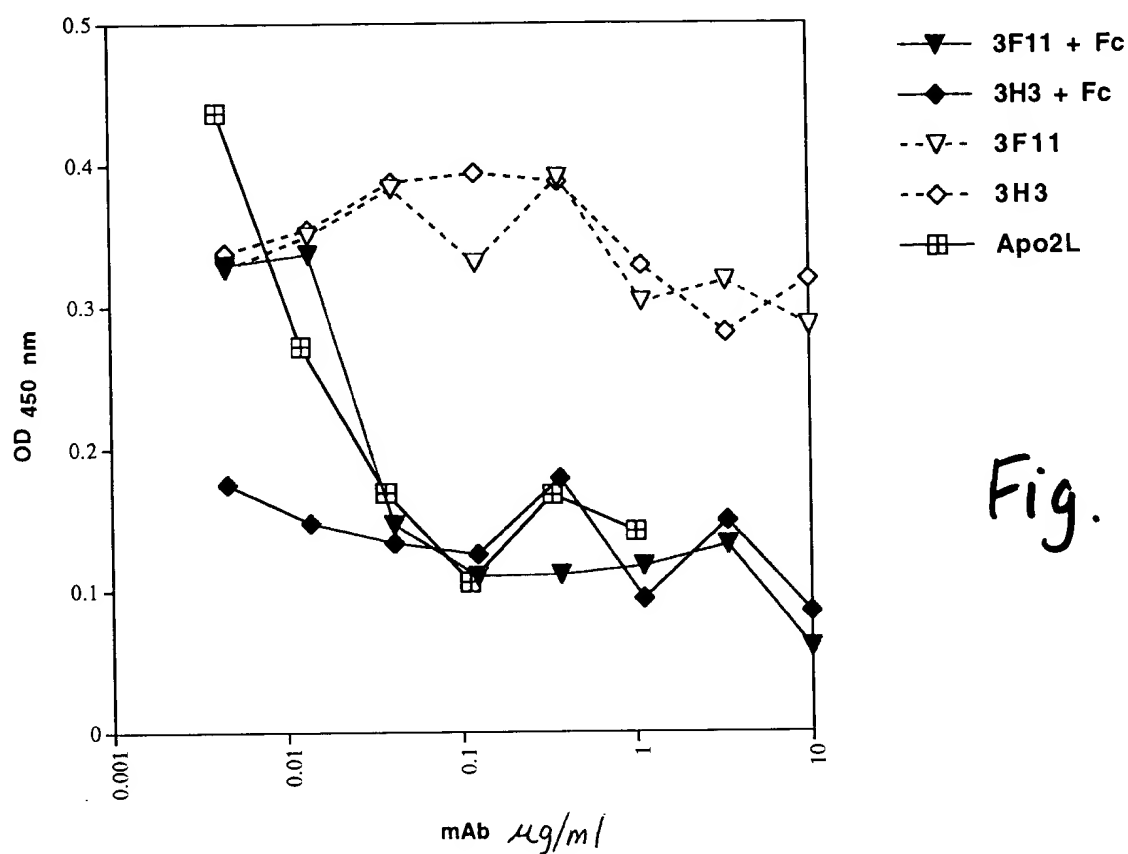
		Affinity (pM)
DR4-IgG	to Apo2L	82
Apo-2 -IgG	to Apo2L	1
mAb 3F11	to Apo-2 IgG	20
mAb 3H3	to "	3

Fig. 13

09396710 " 091599

Fig. 14





665160" DT 296660

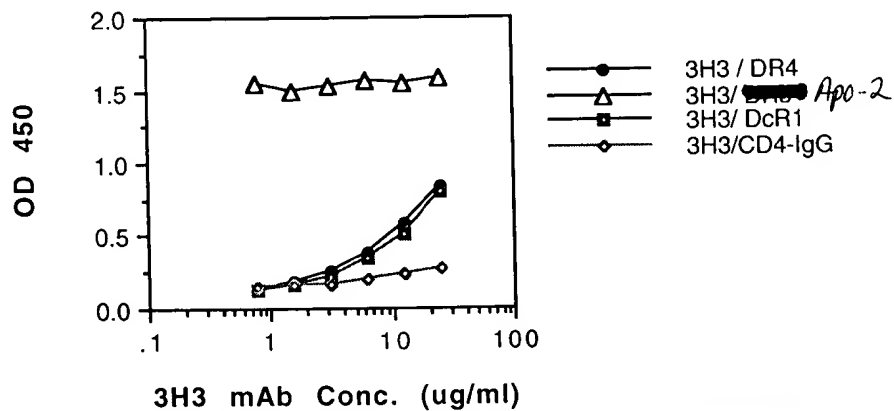
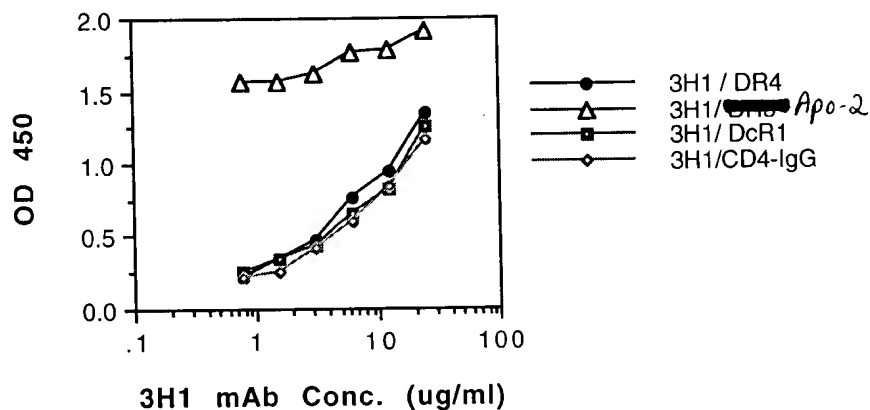
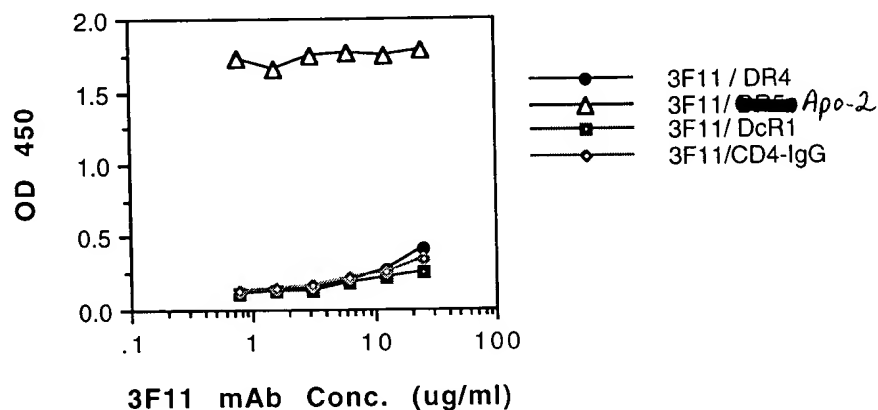
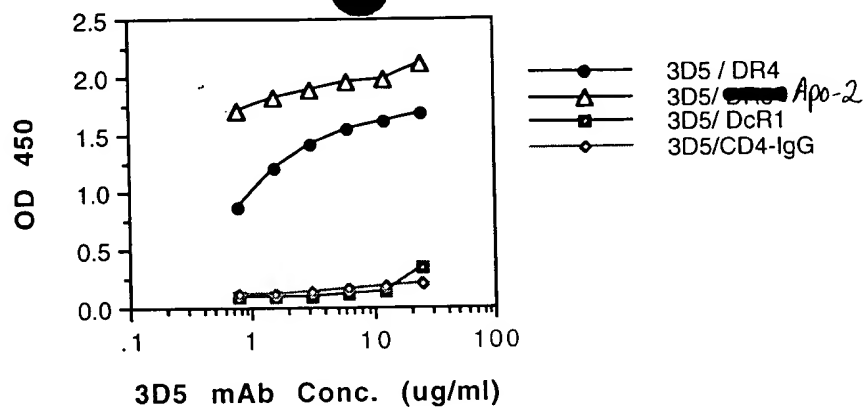


Fig. 16

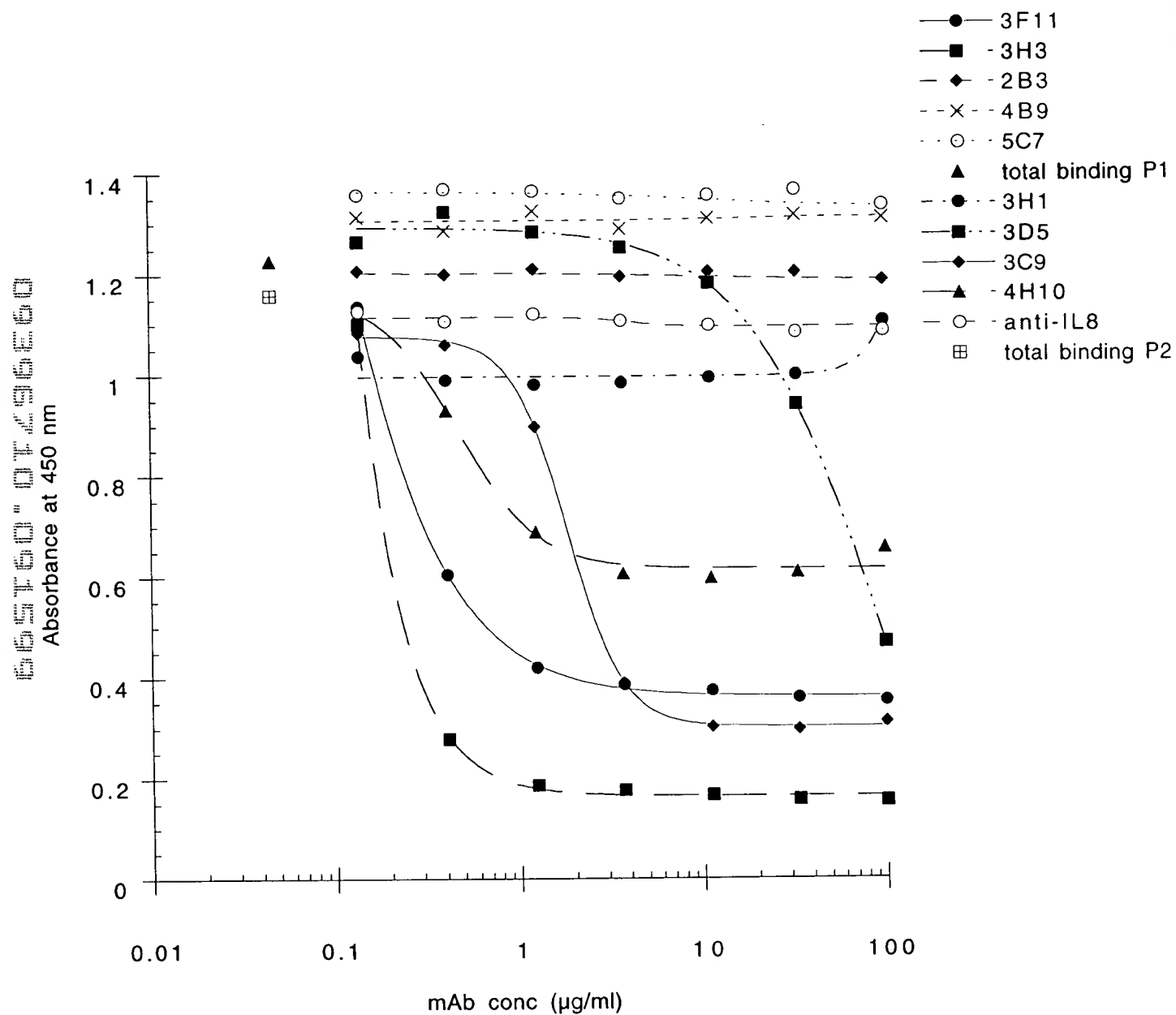


Fig. 17

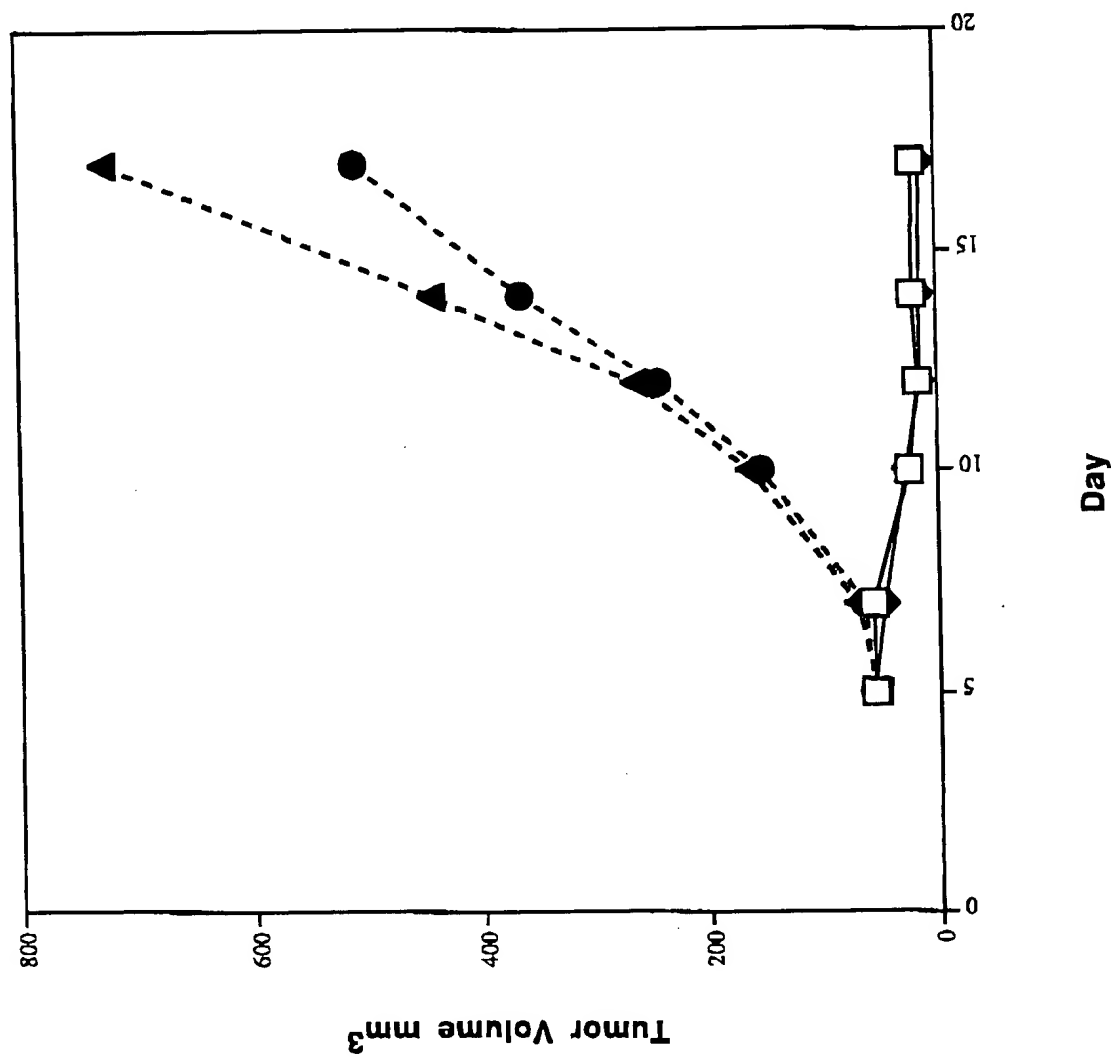


Fig. 18

Data Collection

	In-house	SSRL
Resolution (Å)	30-3.5 (3.62-3.50) ^a	30-2.4 (2.49-2.40) ^a
R _{sym} ^b	0.185 (0.398) ^a	0.056 (0.396) ^a
Number of observations	51,527	152,986
Unique reflections	12,459	38,908
Completeness (%)	99.8 (99.9) ^a	99.8 (99.7) ^a

Refinement

Resolution (Å)	30-2.4
Number of reflections	38,850
Final R ^c , R _{free} (F>0)	0.222, 0.267
Number of residues	781
Number of solvent molecules	286
Number of non-H atoms	6577
Average B factor (Å ²)	47.6
Rmsd bonds (Å)	0.013
Rmsd angles (°)	1.7
Rmsd B (bonded atoms) (Å ²)	2.4

^a Numbers in parentheses refer to the highest resolution shell.

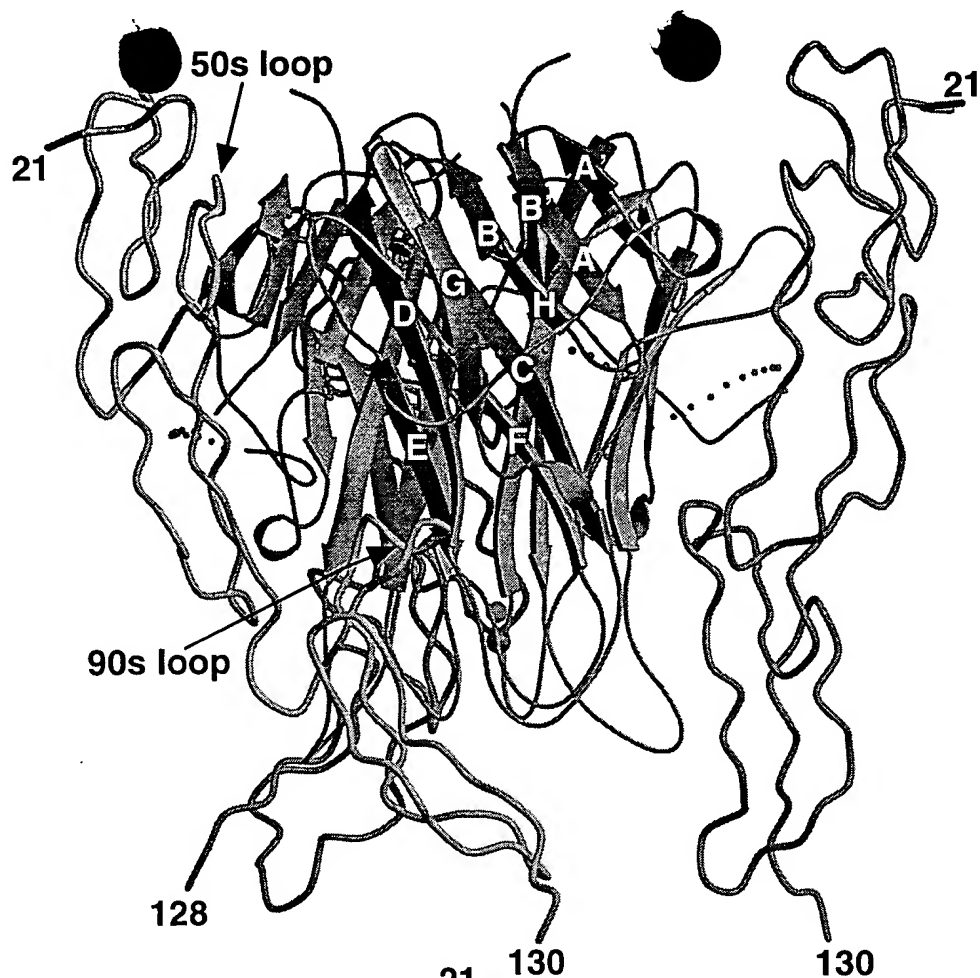
^b $R_{sym} = \sum ||\langle I \rangle| / \sum I$. $\langle I \rangle$ is the average intensity of symmetry related observations of a unique reflection.

^c $R = \sum |F_o - F_c| / \sum F_o$. R_{free} is calculated as R, but for 10% of the reflections excluded from all refinement.

Fig. 19

09396710.091599 665160"01296E6D

A



B

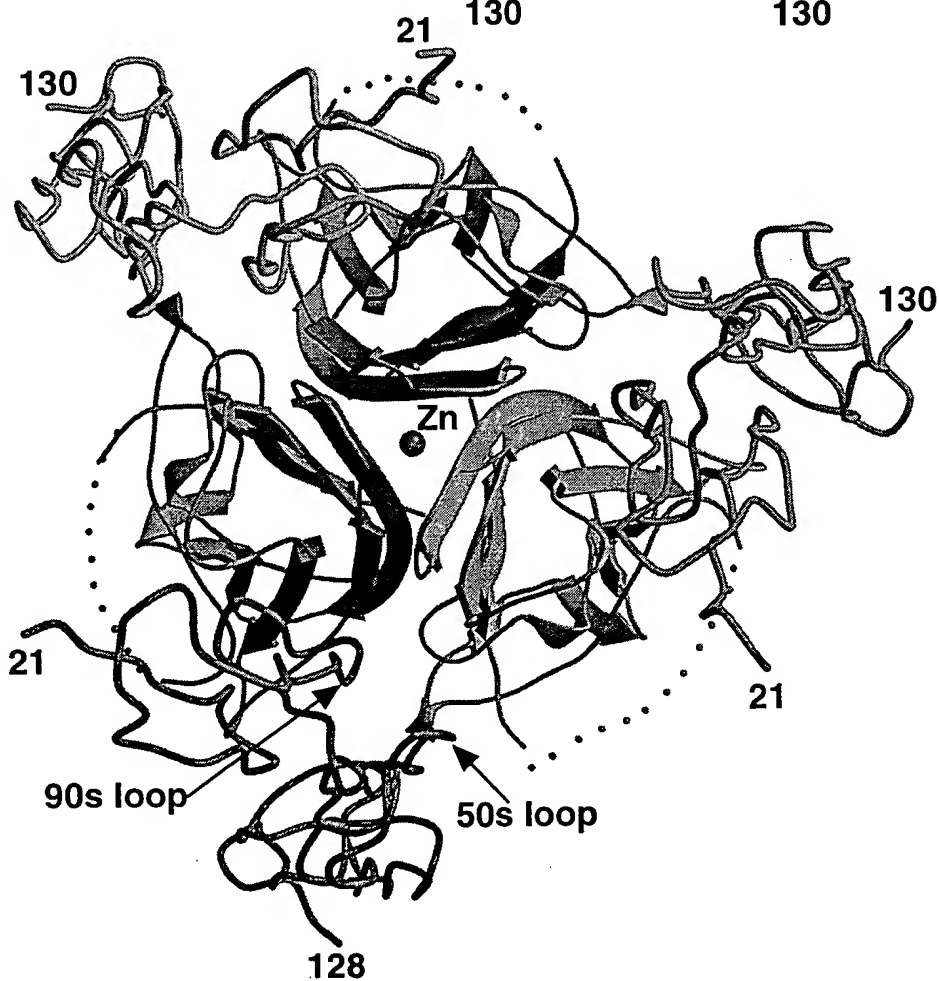


Figure 20

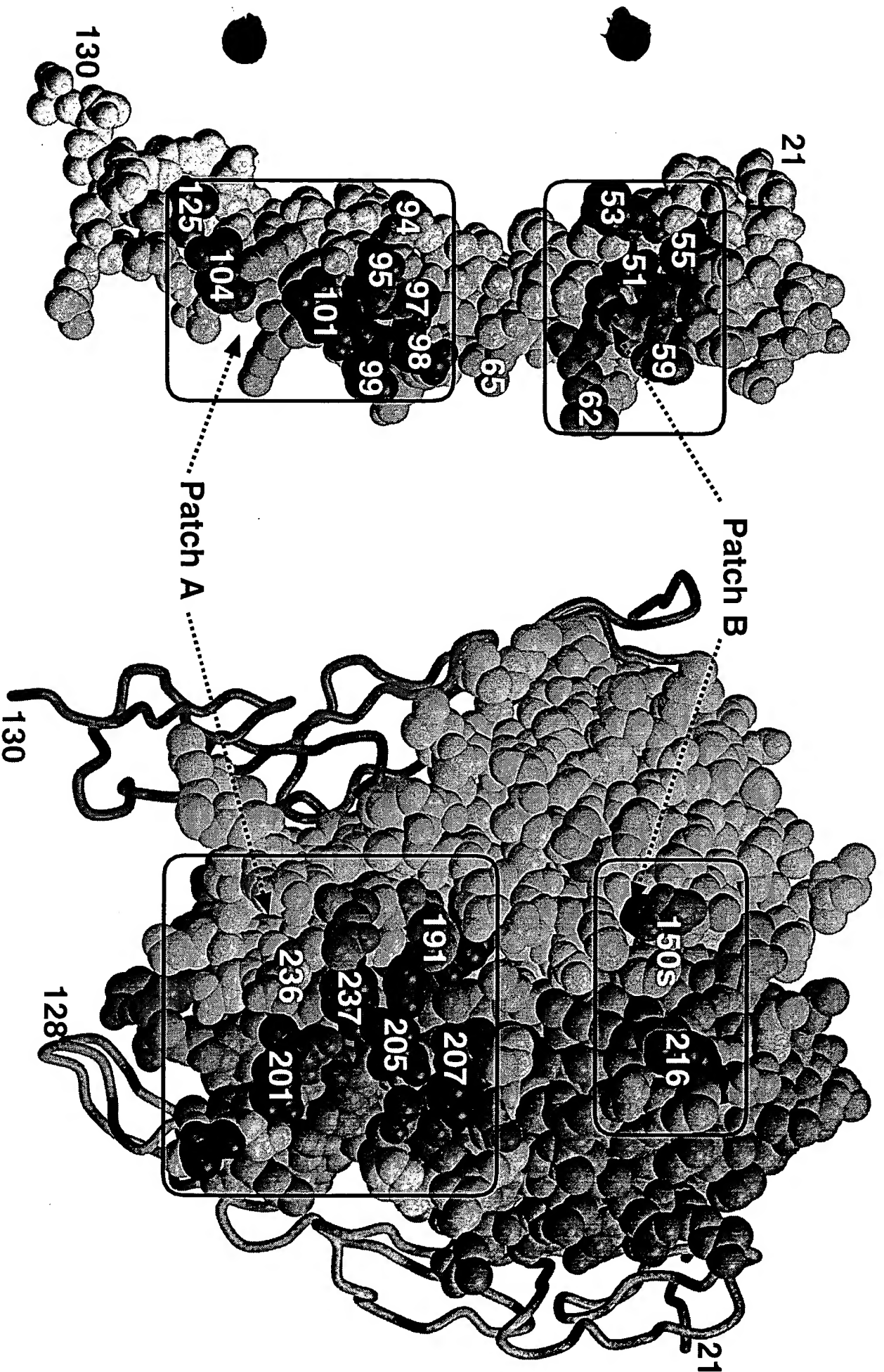


Figure 21